

REIVED

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JUL 16 2003

ENTER 1600/2900



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/873,106C

DATE: 07/10/2003

TIME: 15:30:17

Input Set : A:\1062.1021-004.txt

Output Set: N:\CRF4\07102003\I873106C.raw

4 <110> APPLICANT: Reinherz, Ellis L.  
5 Freund, Christian  
6 Li, Jing  
7 Nishizawa, Kazuhisa  
8 Wagner, Gerhard  
10 <120> TITLE OF INVENTION: Cloning and Characterization of a CD2  
11 Binding Protein (CD2BP2)  
14 <130> FILE REFERENCE: 1062.1021-004  
16 <140> CURRENT APPLICATION NUMBER: 09/873,106C  
17 <141> CURRENT FILING DATE: 2001-06-01  
19 <150> PRIOR APPLICATION NUMBER: US 60/111,007  
20 <151> PRIOR FILING DATE: 1998-12-04  
22 <150> PRIOR APPLICATION NUMBER: US 60/115,647  
23 <151> PRIOR FILING DATE: 1999-01-13  
25 <150> PRIOR APPLICATION NUMBER: PCT/US99/26993  
26 <151> PRIOR FILING DATE: 1999-11-15  
28 <160> NUMBER OF SEQ ID NOS: 25  
30 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
32 <210> SEQ ID NO: 1  
33 <211> LENGTH: 1299  
34 <212> TYPE: DNA  
35 <213> ORGANISM: Homo sapiens  
37 <220> FEATURE:  
38 <221> NAME/KEY: CDS  
39 <222> LOCATION: (121)...(1143)  
41 <400> SEQUENCE: 1  
42 agtcctcttc cgggtatgg cggcggtgc cccggatgta gccctggcgc aagcatctct 60  
43 tctttttcc acctcgccctt ccgcggattc ccagctttag aaacacctct ttgccccgtc 120  
44 atg cca aag agg aaa gtg acc ttc caa ggc gtg gga gat gag gag gat 168  
45 Met Pro Lys Arg Lys Val Thr Phe Gln Gly Val Gly Asp Glu Glu Asp  
46 1 5 10 15  
48 gag gat gaa atc att gtc ccc aag aag ctg gtg gac cct gtg gct 216  
49 Glu Asp Glu Ile Ile Val Pro Lys Lys Lys Leu Val Asp Pro Val Ala  
50 20 25 30  
52 ggg tca ggg ggt cct ggg agc cgc ttt aaa ggc aaa cac tct ttg gat 264  
53 Gly Ser Gly Gly Pro Gly Ser Arg Phe Lys Gly Lys His Ser Leu Asp  
54 35 40 45  
56 agc gat gag gag gat gat gat gat ggg ggg tcc agc aaa tat gac 312  
57 Ser Asp Glu Glu Asp Asp Asp Gly Gly Ser Ser Lys Tyr Asp  
58 50 55 60  
60 atc ttg gcc tca gag gat gta gaa ggt cag gag gca gcc aca ctc ccc 360  
61 Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro  
62 65 70 75 80

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64	agc	gag	ggg	ggt	cggt	atc	aca	ccc	ttt	aac	ctg	cag	gag	gag	atg	408		
65	Ser	Glu	Gly	Gly	Gly	Arg	Ile	Thr	Pro	Phe	Asn	Leu	Gln	Glu	Glu	Met		
66							85				90				95			
68	gag	gaa	ggc	cac	ttt	gat	gcc	gat	ggc	aac	tac	ttc	ctg	aac	cggt	456		
69	Glu	Glu	Gly	His	Phe	Asp	Ala	Asp	Gly	Asn	Tyr	Phe	Leu	Asn	Arg	Asp		
70							100				105				110			
72	gct	cag	atc	cga	gac	agc	tgg	ctg	gac	aac	att	gac	tgg	gtg	aag	atc	504	
73	Ala	Gln	Ile	Arg	Asp	Ser	Trp	Leu	Asp	Asn	Ile	Asp	Trp	Val	Lys	Ile		
74							115				120				125			
76	cgg	gag	cggt	cca	cct	ggc	cag	cggt	cag	gcc	tca	gac	tcg	gag	gag	gag	552	
77	Arg	Glu	Arg	Pro	Pro	Gly	Gln	Arg	Gln	Ala	Ser	Asp	Ser	Glu	Glu	Glu		
78							130				135				140			
80	gac	agc	ttt	ggc	cag	acc	tca	atg	agt	gcc	caa	gcc	ctc	ttt	gag	gga	600	
81	Asp	Ser	Leu	Gly	Gln	Thr	Ser	Met	Ser	Ala	Gln	Ala	Leu	Leu	Glu	Gly		
82	145						150				155				160			
84	ctt	ttt	gag	ctc	cta	ttt	cct	aga	gag	aca	gtt	gct	ggg	gca	ctg	agg	648	
85	Leu	Leu	Glu	Leu	Leu	Pro	Arg	Glu	Thr	Val	Ala	Gly	Ala	Leu	Arg			
86							165				170				175			
88	cgt	ctg	ggg	gcc	cga	gga	ggc	aaa	ggg	aga	aag	ggg	cct	ggg	caa		696	
89	Arg	Leu	Gly	Ala	Arg	Gly	Gly	Gly	Lys	Gly	Arg	Lys	Gly	Pro	Gly	Gln		
90							180				185				190			
92	ccc	agt	tcc	cct	cag	cggt	ctg	gac	cggt	ctc	tcc	ggg	ttt	gcc	gac	cag	744	
93	Pro	Ser	Ser	Pro	Gln	Arg	Leu	Asp	Arg	Leu	Ser	Gly	Leu	Ala	Asp	Gln		
94							195				200				205			
96	atg	gtt	gcc	cggt	ggc	aac	ctt	ggt	gtt	tac	cag	gaa	aca	agg	gaa	cggt	792	
97	Met	Val	Ala	Arg	Gly	Asn	Leu	Gly	Val	Tyr	Gln	Glu	Thr	Arg	Glu	Arg		
98							210				215				220			
100	ttt	ttt	gtt	atg	cgt	ctg	aag	gggt	ttt	gggt	tgt	cag	acc	cta	gga	ccc	cac	840
101	Leu	Ala	Met	Arg	Leu	Lys	Gly	Leu	Gly	Cys	Gln	Thr	Leu	Gly	Pro	His		
102	225						230				235				240			
104	aat	ccc	aca	ccc	cca	ccc	tcc	ctg	gac	atg	ttt	gct	gag	gag	ttt	gct	888	
105	Asn	Pro	Thr	Pro	Pro	Ser	Leu	Asp	Met	Phe	Ala	Glu	Glu	Leu	Ala			
106							245				250				255			
108	gag	gag	gaa	ctg	gag	acc	cca	acc	cct	acc	cag	aga	gga	gaa	gca	gag	936	
109	Glu	Glu	Glu	Leu	Glu	Thr	Pro	Thr	Pro	Thr	Gln	Arg	Gly	Glu	Ala	Glu		
110							260				265				270			
112	tcg	cggt	ggat	gggt	ctg	gtt	gtt	gtt	atg	tgg	gaa	tat	aag	tgg	gag		984	
113	Ser	Arg	Gly	Asp	Gly	Leu	Val	Asp	Val	Met	Trp	Glu	Tyr	Lys	Trp	Glu		
114							275				280				285			
116	aac	acg	ggg	gat	gcc	gag	ctg	tat	ggg	ccc	ttt	acc	agc	gcc	cag	atg	1032	
117	Asn	Thr	Gly	Asp	Ala	Glu	Leu	Tyr	Gly	Pro	Phe	Thr	Ser	Ala	Gln	Met		
118							290				295				300			
120	cag	acc	tgg	gtt	agt	gaa	ggc	tac	ttt	ccg	gac	ggt	gtt	tat	tgc	cggt	1080	
121	Gln	Thr	Trp	Val	Ser	Glu	Gly	Tyr	Phe	Pro	Asp	Gly	Val	Tyr	Cys	Arg		
122	305						310				315				320			
124	aag	ctg	gac	ccc	cct	ggt	ggt	cag	ttt	tac	aac	tcc	aaa	cgc	att	gac	1128	
125	Lys	Leu	Asp	Pro	Pro	Gly	Gly	Gln	Phe	Tyr	Asn	Ser	Lys	Arg	Ile	Asp		
126							325				330				335			
128	ttt	gac	ctc	tac	acc	tgagcctgct	ggggggccca	gg	ttt	gg	ttt	cc	ttt	ttt	cc	cc	1183	

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129 Phe Asp Leu Tyr Thr  
130 340  
132 tggactttgt ggaggaggca ccaagtgtct caggcagcga ggaaatttggaa ggccattttt 1243  
133 cagtcaattt ccctttccca ataaaaggct tagttgtgtaa aaaaaaaaaa aaaaaaa 1299  
135 <210> SEQ ID NO: 2  
136 <211> LENGTH: 341  
137 <212> TYPE: PRT  
138 <213> ORGANISM: Homo sapiens  
140 <400> SEQUENCE: 2  
141 Met Pro Lys Arg Lys Val Thr Phe Gln Gly Val Gly Asp Glu Glu Asp  
142 1 5 10 15  
143 Glu Asp Glu Ile Ile Val Pro Lys Lys Lys Leu Val Asp Pro Val Ala  
144 20 25 30  
145 Gly Ser Gly Gly Pro Gly Ser Arg Phe Lys Gly Lys His Ser Leu Asp  
146 35 40 45  
147 Ser Asp Glu Glu Asp Asp Asp Gly Ser Ser Lys Tyr Asp  
148 50 55 60  
149 Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro  
150 65 70 75 80  
151 Ser Glu Gly Gly Arg Ile Thr Pro Phe Asn Leu Gln Glu Glu Met  
152 85 90 95  
153 Glu Glu Gly His Phe Asp Ala Asp Gly Asn Tyr Phe Leu Asn Arg Asp  
154 100 105 110  
155 Ala Gln Ile Arg Asp Ser Trp Leu Asp Asn Ile Asp Trp Val Lys Ile  
156 115 120 125  
157 Arg Glu Arg Pro Pro Gly Gln Arg Gln Ala Ser Asp Ser Glu Glu  
158 130 135 140  
159 Asp Ser Leu Gly Gln Thr Ser Met Ser Ala Gln Ala Leu Leu Glu Gly  
160 145 150 155 160  
161 Leu Leu Glu Leu Leu Pro Arg Glu Thr Val Ala Gly Ala Leu Arg  
162 165 170 175  
163 Arg Leu Gly Ala Arg Gly Gly Lys Gly Arg Lys Gly Pro Gly Gln  
164 180 185 190  
165 Pro Ser Ser Pro Gln Arg Leu Asp Arg Leu Ser Gly Leu Ala Asp Gln  
166 195 200 205  
167 Met Val Ala Arg Gly Asn Leu Gly Val Tyr Gln Glu Thr Arg Glu Arg  
168 210 215 220  
169 Leu Ala Met Arg Leu Lys Gly Leu Gly Cys Gln Thr Leu Gly Pro His  
170 225 230 235 240  
171 Asn Pro Thr Pro Pro Ser Leu Asp Met Phe Ala Glu Glu Leu Ala  
172 245 250 255  
173 Glu Glu Glu Leu Glu Thr Pro Thr Pro Gln Arg Gly Glu Ala Glu  
174 260 265 270  
175 Ser Arg Gly Asp Gly Leu Val Asp Val Met Trp Glu Tyr Lys Trp Glu  
176 275 280 285  
177 Asn Thr Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met  
178 290 295 300  
179 Gln Thr Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly Val Tyr Cys Arg  
180 305 310 315 320

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Input Set : A:\1062.1021-004.txt  
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181 Lys Leu Asp Pro Pro Gly Gly Gln Phe Tyr Asn Ser Lys Arg Ile Asp  
182 325 330 335  
183 Phe Asp Leu Tyr Thr  
184 340  
187 <210> SEQ ID NO: 3  
188 <211> LENGTH: 26  
189 <212> TYPE: PRT  
190 <213> ORGANISM: Homo sapiens  
192 <400> SEQUENCE: 3  
193 Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met Gln Thr  
194 1 5 10 15  
195 Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly  
196 20 25  
199 <210> SEQ ID NO: 4  
200 <211> LENGTH: 27  
201 <212> TYPE: PRT  
202 <213> ORGANISM: Caenorhabditis elegans  
204 <400> SEQUENCE: 4  
205 Gly Pro Asp Ser Glu Lys Tyr Gly Pro Tyr Met Ser Lys Asp Met Leu  
206 1 5 10 15  
207 Phe Trp Leu Gln Ala Gly Tyr Phe Asn Asp Gly  
208 20 25  
211 <210> SEQ ID NO: 5  
212 <211> LENGTH: 27  
213 <212> TYPE: PRT  
214 <213> ORGANISM: Caenorhabditis elegans  
216 <400> SEQUENCE: 5  
217 Asp Pro Thr Glu Thr Arg Arg Gly Pro Phe Pro Lys Asp Gln Met Asn  
218 1 5 10 15  
219 Val Trp Phe Lys Ala Gly Tyr Phe Thr Asp Glu  
220 20 25  
223 <210> SEQ ID NO: 6  
224 <211> LENGTH: 27  
225 <212> TYPE: PRT  
226 <213> ORGANISM: Caenorhabditis elegans  
228 <400> SEQUENCE: 6  
229 Asp Asp Arg Gly Thr Val Gln Gly Pro Tyr Gly Ala Ser Thr Val Leu  
230 1 5 10 15  
231 Asp Trp Tyr Gln Lys Gly Tyr Phe Ser Asp Asn  
232 20 25  
235 <210> SEQ ID NO: 7  
236 <211> LENGTH: 29  
237 <212> TYPE: PRT  
238 <213> ORGANISM: Saccharomyces cerevisiae  
240 <400> SEQUENCE: 7  
241 Asp Thr Gln Gly Gln Ile His Gly Pro Phe Thr Thr Gln Met Met Ser  
242 1 5 10 15  
243 Gln Trp Tyr Ile Gly Gly Leu Glu Tyr Phe Ala Ser Thr  
244 20 25

RAW SEQUENCE LISTING DATE: 07/10/2003  
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Input Set : A:\1062.1021-004.txt  
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247 <210> SEQ ID NO: 8  
248 <211> LENGTH: 27  
249 <212> TYPE: PRT  
250 <213> ORGANISM: *Saccharomyces cerevisiae*  
252 <400> SEQUENCE: 8  
253 Asp Ser Asn Gly Asn Ile Gln Gly Pro Phe Gly Thr Asn Asn Met Ser  
254 1 5 10 15  
255 Gln Trp Tyr Gln Gly Gly Tyr Phe Thr Pro Thr  
256 20 25  
259 <210> SEQ ID NO: 9  
260 <211> LENGTH: 17  
261 <212> TYPE: PRT  
262 <213> ORGANISM: Artificial Sequence  
264 <220> FEATURE:  
265 <223> OTHER INFORMATION: Motif in CD2 binding region of CD2BP2  
W--> 268 <221> NAME/KEY: VARIANT  
269 <222> LOCATION: 1,2,4,5,6,7,9,10,11,12,13,14,15  
270 <223> OTHER INFORMATION: Xaa = Any Amino Acid  
W--> 272 <221> VARIANT  
273 <222> LOCATION: 3  
274 <223> OTHER INFORMATION: Xaa can be Tyr or Phe  
W--> 276 <221> VARIANT  
277 <222> LOCATION: 8  
278 <223> OTHER INFORMATION: Xaa can be Met or Val  
W--> 280 <400> 9  
W--> 281 Gly Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Xaa Xaa Xaa Gly Tyr  
282 1 5 10 15  
283 Phe  
287 <210> SEQ ID NO: 10  
288 <211> LENGTH: 6  
289 <212> TYPE: PRT  
290 <213> ORGANISM: Artificial Sequence  
292 <220> FEATURE:  
293 <223> OTHER INFORMATION: CD2BP2 binding region  
296 <400> SEQUENCE: 10  
297 Pro Pro Pro Gly His Arg  
298 1 5  
301 <210> SEQ ID NO: 11  
302 <211> LENGTH: 70  
303 <212> TYPE: PRT  
304 <213> ORGANISM: *Homo sapiens*  
306 <400> SEQUENCE: 11  
307 Pro Pro Pro Pro Gly His Arg Ser Gln Ala Pro Ser His Arg Pro  
308 1 5 10 15  
309 Pro Pro Pro Gly His Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro  
310 20 25 30  
311 Ala Pro Ser Gly Thr Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro  
312 35 40 45  
313 Arg Pro Arg Val Gln Pro Lys Pro Pro His Gly Ala Ala Glu Asn Ser

RAW SEQUENCE LISTING ERROR SUMMARY                    DATE: 07/10/2003  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; Xaa Pos. 3,4,5,6,7,8,9,10,12,13,14

**VERIFICATION SUMMARY**

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L:268 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:272 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9  
L:276 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9  
L:280 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9  
L:281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0